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**Modulation of the immune system by the gut microbiota in the development of Type
1 Diabetes**

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Abstract

T1D is an autoimmune disease characterized by T cell-mediated destruction of insulin-producing β -cells in the pancreatic islets of Langerhans, resulting in hyperglycemia, with patients requiring lifelong insulin treatment. Many studies have shown that genetics alone are not sufficient for the increase in T1D incidence and thus other factors have been suggested to modify the disease risk. T1D incidence has sharply increased in the developed world, especially amongst youth¹. In Europe, T1D incidence is increasing at an annual rate of 3-4%². Increasing evidence shows that gut microbiota, as one of the environmental factors influencing diabetes development, play an important role in development of T1D³. Here, we summarize the current knowledge about the relationship between the microbiota and T1D. We also discuss the possibility of T1D prevention by changing the composition of gut microbiota.

Introduction

The elucidation of the complex interactions between the gut microbiota, metabolism, and the immune system may lead to groundbreaking changes as to how specific diseases are prevented and treated. The gut microbiota refers to the community of bacteria located within the intestine that have coevolved through millions of years with the host. This symbiotic relationship is important for many host functions including digestion, nutrient acquisition, and the development of the immune system⁴.

The gut microbiota encodes trillions of genes, of which approximately 5-10 million are unique⁵⁻⁷. In total, there are ~150 times more genes than in the human genome⁶. In healthy humans, the number of the bacteria increases exponentially from the small intestine to the colon; thus, the colon is the main contributor to the total bacterial population in the gut⁸. The main commensal bacterial phyla in the gut microbiota include, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Proteobacteria*, and *Verrucomicrobia* with the vast majority consisting of *Bacteroidetes* and *Firmicutes*.

The gut microbiota of each individual host is diverse and unique⁹. For maintenance of good health, there is a natural balance between the host and its microbial community. However, dysbiosis, which is a disturbance in the balance between the host and the microbial community, is associated with various chronic diseases, including

obesity, inflammatory bowel disease (IBD), type 1 diabetes (T1D) and type 2 diabetes (T2D)¹⁰.

Recent evidence suggests the gut microbiota may begin colonization *in utero* as bacteria have been detected in the intrauterine environment including the amniotic fluid¹¹, placenta¹², meconium¹³, and the umbilical cord¹⁴. While the majority of these studies utilize 16S rRNA sequencing or PCR, in a small number the investigators have grown bacteria by culturing the amniotic fluid¹¹ or the umbilical cord¹⁴ samples in different bacterial culture conditions. In addition, the development of the gut microbiota can be influenced by the delivery mode. Infants delivered by Caesarean section (C-section) exhibit less bacterial diversity up to 2 years after birth compared with those delivered vaginally¹⁵. C-section deliveries have also been associated with an increased risk of obesity¹⁶ or T1D¹⁷ later in life, which may be linked to the fact that the gut microbiota continue to develop into adulthood¹⁸. This potentially provides a greater window of opportunity for therapeutic modulation of the gut microbiota.

There are many ways that the gut microbiota can be modified, including the environments we live in (e.g. rural or urban), diet and food supplements (probiotics), the use of antibiotics or other medications during illness. Other factors, such as age and gender, can also modify the microbial composition over time. For example, the healthy pediatric gut microbiota exhibit significant compositional and functional differences from those of adults¹⁸. It has been shown that children had increased abundances of *Bifidobacterium*, *Faecalibacterium*, and *Lachnospiraceae* compared with adults, while adults had increased abundance of *Bacteroides*⁴. Currently, it is not clear what constitutes a “healthy” gut microbial composition; however, the microbiota are indispensable for the digestion of nutrients¹⁹, development of mucosal immunity²⁰, and supporting gut-brain communication²¹. Furthermore, a loss of diversity in the gut microbiota or alterations in microbial functions have been associated with risk of developing chronic diseases including T1D and other autoimmune or inflammatory disorders. Therefore, developing or retaining a “healthy” microbiota is important.

T1D is an autoimmune disease characterized by T cell-mediated destruction of insulin-producing β -cells in the pancreatic islets of Langerhans, resulting in hyperglycemia, with patients requiring lifelong insulin treatment. Many studies have

1 shown that genetics alone are not sufficient for the increase in T1D incidence and thus
2 other factors have been suggested to modify the disease risk. T1D incidence has sharply
3 increased in the developed world, especially amongst youth¹. In Europe, T1D incidence
4 is increasing at an annual rate of 3-4%². Increasing evidence shows that gut microbiota,
5 as one of the environmental factors influencing diabetes development, play an important
6 role in development of T1D³. Here, we summarize the current knowledge about the
7 relationship between the microbiota and T1D. We also discuss the possibility of T1D
8 prevention by changing the composition of gut microbiota.

10 **Animal Models of T1D**

11 To gain the best knowledge of the mechanism(s) of a disease development, the
12 ideal studies are *in vivo* investigations. For ethical reasons, there are considerable
13 limitations to *in vivo* studies in humans. However, animal models of human diseases
14 provide an alternative system to investigate the mechanism behind the immune response
15 within the pancreas, in the case of T1D, or the bacteria in the gut, *in vivo*, to answer
16 questions that we cannot do in humans. Utilizing bench to bedside and bedside to bench
17 approaches can further expand our understanding and help us to achieve the ultimate goal
18 of preventing T1D development or to develop a cure.

19 There are two widely used rodent models for human T1D research - the non-
20 obese diabetic (NOD) mouse²² and the bio-breeding (BB) rat²³. Both the NOD mouse
21 and the BB rat develop spontaneous T1D, similar to humans. NOD mice usually develop
22 T1D after 10 weeks of age²⁴, while BB rats develop T1D from 7 to 14 weeks²⁵. In
23 affected humans, the age of onset of T1D typically ranges from 6 months to late
24 adolescence. The NOD mouse and the BB rat also carry the T1D susceptibility major
25 histocompatibility complex (MHC) class II genes, similar to the human T1D
26 susceptibility MHCII alleles. The NOD mouse recapitulates many features of human
27 T1D, especially those T1D susceptibility genes²⁶. However, the pathogenesis of T1D in
28 both humans and animal models is not solely determined by genetics; the disease onset is
29 influenced by a combination of genetic and environmental factors. Pathologically,
30 humans²⁷, the BB rat²⁸ and NOD mice²⁹ display infiltration of lymphocytes in the
31 pancreas, namely, insulitis. The immune cells that are involved in the destruction of

insulin-producing beta cells in humans, are similar to those cells present in NOD mice and BB rats during diabetes development. These cells are mainly autoreactive T cells as T1D is a T cell-mediated disease. Furthermore, the autoantigens that the T cell recognizes in human T1D are also present in the NOD mouse³⁰. In humans, a gender bias emerges after puberty with a small increase in the number of affected males³¹, while the majority of diabetic NOD mice are females²². However, there is no gender bias in T1D development in BB rats²³.

Unlike human studies, studies using animal models can be better controlled in order to minimize variables and assess the effect of different environmental factors, such as diet, mode of birth delivery and usage of medication, on the gut microbiota and the development of T1D. Therefore, studies using animal models provide an extremely valuable and unique tool for gaining more insightful knowledge about the disease. In addition, humans³² and rodents^{33, 34} with T1D have been shown to exhibit similar gastroenterological abnormalities, including increased intestinal permeability, altered microvilli, leaky tight junctions, and altered gut microbiota³⁵⁻³⁷. Similar to humans, *Bacteroidetes* and *Firmicutes* are also the dominant phyla in relation to the composition of gut microbiota. However, there are also major differences as 85% of the bacterial genera found in mice are absent in humans³⁸. Moreover, a disadvantage of well-controlled studies using in-bred animal models may be a lack of direct translation to humans, who are extremely heterogeneous.

Gut Microbiota and T1D

Hygiene Hypothesis

The concept of the gut microbiota as a major environmental factor influencing T1D supports the rising incidence rates in developed countries. The hygiene hypothesis originally was coined in relation to observations of respiratory problems, hygiene and household size³⁹. A modification of this may help to explain the increased T1D incidence as a result of reduced diversity in the microbiota. The sharp increase in T1D incidence dates back to the mid 20th century where children were raised in environments with increased levels of sanitation and thus have less exposure to bacteria and parasites.

1 The hygiene hypothesis has been tested in NOD mice, as the cleaner the living
2 conditions, the higher the incidence of diabetes found in NOD mice⁴⁰. Moreover, studies
3 have found that infection of NOD mice early in life with a number of different bacteria
4 can prevent T1D^{41, 42}. Human epidemiological studies showed that the incidence of T1D
5 and allergies is much lower in developing countries where the living standard is low but
6 the rate of bacterial or parasite infection is high⁴³. Links found between gut microbiota
7 and T1D, discussed in this review, have prompted questions on how the gut microbiota
8 can be modulated in order to alter T1D development.

10 Gut Microbiota in T1D

11 Both the gut microbiota composition and the immune system co-evolve and
12 develop together over time, and young children have reduced microbial diversity and a
13 less mature immune system compared to adults^{18, 44}. Therefore, it is important to
14 understand how the gut microbiota interacts with the immune system and further, how
15 these interactions alter susceptibility to T1D. Roesch and colleagues found that bacteria
16 of the *Bacteroides* genus were more common in diabetes-prone BB rats (BB-DP) than
17 they were in diabetes-resistant BB rats (BB-DR)⁴⁵. However, the abundance of bacteria
18 belonging to the *Lactobacillus* and *Bifidobacterium* genera was higher in BB-DR rats
19 than in BB-DP rats⁴⁵. Altered microbiota were also found between the NOD mouse and
20 non-obese diabetes resistant (NOR) mouse⁴⁶. According to Daft and colleagues, the
21 NOD mouse has a lower *Firmicutes:Bacteroidetes* ratio as well as a lower abundance of
22 *Prevotella* compared to the NOR mouse⁴⁶. This profile is also seen in children with T1D
23 compared to age-matched healthy children³⁷. Long-term changes in the gut microbiota of
24 NOD or NOR mice can be accomplished by cross-fostering, whereby NOD mice are
25 nursed by NOR mothers and vice versa⁴⁶. Cross-fostering of NOD mice results in both
26 the loss of some diabetogenic bacteria and the gain of bacteria associated with diabetes
27 protection. Further, NOD mice fostered by NOR mothers had a decreased incidence of
28 T1D⁴⁶.

29 Gut microbiota can modulate T1D susceptibility associated with known T1D
30 susceptibility loci. Genetic susceptibility at the MHC loci is the most important risk
31 factor for T1D development in both NOD mice and humans. NOD mice express the gene

1 encoding MHC class II IA^{g7}, which is a homolog of human HLA-DQ8⁴⁷⁻⁴⁹. NOD mice
2 do not express IE, another MHC class II gene, a homolog of human HLA-DR^{48, 49}.
3 Expression of IE, or expression of IA^b, the MHC class II locus for C57BL/6 mice, instead
4 of IA^{g7}, is associated with protection from disease in NOD mice^{50, 51}. Interestingly, a
5 recent study by Silverman *et al.* suggested the mechanism of disease protection is
6 mediated by gut microbiota in IE-expressing NOD mice⁵². The authors showed that
7 expression of the IE transgene results in the compositional changes in gut microbiota
8 which contributes to T1D protection. To prove that the disease protection was indeed
9 mediated by the gut microbiota, the authors treated the IE transgenic NOD mice with
10 different antibiotics. Administration of vancomycin or metronidazole, but not neomycin
11 or ampicillin, in the drinking water, disturbed the gut microbiota sufficiently to induce
12 insulinitis in the normally insulinitis-free IE transgenic NOD mice⁵². However, although the
13 presence of IA^b in NOD mice was also able to alter the gut microbiota composition, the
14 effect on diabetes development was minimal⁵³. Expression of other T1D protective
15 genetic loci *Idd3* and/or *Idd5* from C57BL/6 mice in NOD mice^{54, 55} did not lead to
16 changes in gut microbiota but enhanced IL-2 production and Treg function. Mullaney
17 and co-authors further assessed the microbiota from healthy humans carrying the *Idd3/5*
18 protective alleles and found similar gut microbiota composition to NOD mice expressing
19 the same alleles⁵³. These studies not only support the importance of the NOD mouse
20 model of human T1D, but also reveal the importance of the genetic susceptibility loci in
21 T1D, which modulate the interactions of immune cells and gut microbiota.

22 Alterations in the gut microbiota have also been observed in humans with T1D.
23 A study by Giongo and colleagues analyzed bacteria in fecal samples of infants and
24 young children and discovered that children who developed T1D had higher proportions
25 of bacteria from the *Firmicutes* phylum and lower proportions of bacteria in the
26 *Bacteroidetes* phylum than age-matched healthy controls at 4-8 months of age³⁷.
27 However, by the age of 2, children who had developed T1D had a higher proportion of
28 *Bacteroidetes* and a lower proportion of *Firmicutes* relative to healthy controls⁵⁶. Rather
29 than using stool samples, one study compared the duodenal gut microbiota of patients
30 with T1D, or those with celiac disease (CD) and with that of the healthy control
31 subjects³² (due to proximity of the duodenum and close relationship to the pancreas).

1 Some patients with T1D in the study had a gastroduodenal endoscopy and biopsy for CD
2 diagnostic purposes. However, the authors found a distinctive inflammatory profile in
3 the patients with T1D³². Patients with T1D showed overexpression of ten inflammation-
4 associated genes in the biopsies, including chemokines and TNF α , compared to both
5 healthy controls and CD patients³². Further, only patients with T1D exhibited an
6 increased *Firmicutes* and *Firmicutes/Bacteroidetes* ratio but reduced proportion of
7 *Proteobacteria* compared to either patients with CD or healthy controls³².

8 In addition, some studies have investigated the gut microbiota in individuals who
9 are positive for islet autoantibodies and those who are not. In a US-based study, the gut
10 microbiota composition was found to be different between seropositive individuals and
11 their seronegative first-degree relatives (FDRs) with an increased abundance of
12 *Catenibacterium*, *Prevotellaceae* and *RC9 gut group* bacteria in the former⁵⁷.
13 Interestingly, the authors also found that the overall composition of gut microbiota in
14 autoantibody-positive individuals and seronegative FDRs were similar but different from
15 those recent-onset T1D patients and unrelated healthy controls⁵⁷. It is not clear if the
16 FDRs were living in the same or a similar environment; however, this suggests some
17 genetic influence in the composition of gut microbiota and changes in the gut microbiota
18 prior to and/or soon after T1D development. In a European study, Endesfelder and
19 coauthors also compared the composition of gut microbiota between seropositive or
20 seronegative individuals who have an FDR with T1D⁵⁸. Their results did not reveal any
21 differences between autoantibody-positive and -negative individuals in microbiota
22 diversity and composition, as well as single-genus abundance⁵⁸. However, the authors
23 found substantial changes in microbial interaction networks, especially in young children
24 who later developed autoantibodies⁵⁸. In another study, the microbiota composition and
25 alpha diversity in European children, who had seroconverted and later developed
26 diabetes, was different to those who did not seroconvert⁵⁶. In addition, the children who
27 seroconverted but had not developed diabetes by 3 years of age, had a microbiota
28 composition and alpha diversity more similar to non-seroconverters. Together, the data
29 confirmed microbial changes prior to and post-diabetes development. While most studies
30 have focused on 16S rRNA sequencing of the microbiota, Pinto and colleagues
31 investigated the microbial proteome, i.e. the proteins expressed by microbiota isolated

1 from stool samples of healthy children and children with T1D⁵⁹. The authors found that
2 children with T1D had a higher abundance of proteins from *Clostridia* and *Bacteroidetes*,
3 while healthy children had a higher proportion of proteins from *Bifidobacterium*.
4 Although many studies provide evidence of altered gut microbiota in individuals with
5 T1D compared to healthy control subjects, few have shown a causal link between the
6 altered gut microbiota and the disease. However, it is important to note that some of the
7 human studies had very small group sizes, with as few as 3-4 individuals/group^{37, 59}.
8 Thus, larger studies are needed. However, the data from the current human studies
9 suggest that the altered microbiota and their interactions with the immune system are
10 likely to contribute to T1D susceptibility. Therefore, it is important to do functional
11 studies *in vivo* and animal models can provide the perfect tools for this purpose.

12 **Pattern Recognition Receptors**

14 Pattern recognition receptors (PRRs) are germ-line encoded and thus have been
15 conserved over thousands of years to bind conserved structures from pathogens,
16 designated as pathogen-associated molecular patterns (PAMPs), which are present in
17 microorganisms⁶⁰. An example of a PAMP is lipopolysaccharide (LPS), a major
18 component of the outer membrane of gram-negative bacteria⁶¹. There are several PRR
19 families including Toll-like receptors (TLRs) and nucleotide-binding oligomerization
20 domain-like receptors (NLRs).

21 **TLRs**

23 At least 10 and 13 members of the TLR family have been identified in human and
24 mouse, respectively, all of which recognize different PAMPs⁶². TLRs are expressed
25 either on the cell surface (TLR1, 2, 4, 5, 6, 10, 11 and 12) or within the cells (TLR3, 7, 8,
26 9 and 13). TLRs function via signaling through the activation of the NF-κB signaling
27 pathway, inducing proinflammatory cytokines that enable the innate immune system to
28 quickly eradicate potential microbial threats.

29 There are two major TLR signaling pathways mediated by different adaptor
30 proteins, the Myeloid differentiation primary response gene 88 (MyD88) and the Tir-
31 domain-containing adaptor-inducing interferon β protein (TRIF). TLR3, a receptor for

double stranded RNA, relies solely on TRIF signaling, while TLR4, a receptor for LPS, can signal through both MyD88 and TRIF; all the other TLRs rely on MyD88⁶³⁻⁶⁵. Antigen presenting cells (APCs) express many TLRs and play an important role in linking gut microbiota and the host immune system⁶⁶. TLR signaling is essential because it enables optimal antigen presentation by inducing APC maturation and costimulation, as well as the release of cytokines^{61, 65, 67-69}.

TLR interactions with the gut microbiota have been found to be important in contributing to T1D susceptibility. MyD88-deficient (*MyD88*^{-/-}) NOD mice are completely protected from diabetes under normal, specific-pathogen free (SPF) conditions, where gut microbiota are present⁷⁰. However, diabetes was partially restored in the *MyD88*^{-/-}NOD mice after antibiotic administration, suggestive of microbial involvement in the protection of the mice. Interestingly, re-deriving the *MyD88*^{-/-}NOD mice to germ-free (GF) conditions abolished the disease protection. Introduction of commensal bacteria to the GF *MyD88*^{-/-}NOD mice markedly reduced diabetes development. These results demonstrate that MyD88-dependent signaling is important for T1D development, which can be modulated by gut microbiota. Burrows and colleagues reported that diabetes susceptibility in *TLR4*^{-/-}NOD mice and protection in *TLR2*^{-/-}NOD mice were also modulated by gut microbiota⁷¹. LPS recognition has recently drawn more attention in the T1D research field. It is known that Finland has the highest T1D prevalence worldwide, whereas the incidence of T1D in Russia Karelia, a close neighbor of Finland, is six times lower⁷². In addition, there is a greatly reduced risk of developing other autoimmune and allergic diseases in Russian Karelia^{73, 74}. Investigation of the microbiota composition in children living in the different regions revealed that Finnish children had more *Bacteroides* species encoding more LPS synthesis genes, when compared to Russian infants³. Furthermore, the LPS from the *Bacteroides* species isolated from Finnish children was structurally and functionally different from the LPS of *E.coli*, a *Bacteroides* species, found in Russian infants. When the immune function of the two different LPS types in NOD mice was tested, the LPS from *Bacteroides* isolate of the Finnish children was more immunostimulatory than the LPS from the *E.coli* isolate from the Russian children. The finding suggests that altered LPS recognition by TLR4 may be important in modulating susceptibility to T1D.

1 Interestingly, TLR3-deficiency on the NOD background had no impact on diabetes
2 development; however, viral infection models of diabetes development required TLR3 on
3 both the NOD background as well as other genetic backgrounds for diabetes to develop<sup>75-
4 79</sup>. Furthermore, it was noted that enhanced costimulatory molecule expression in the
5 islets, using transgenic constructs directed by the rat insulin promoter, involved changes
6 to the gut microbiota and signaling through TLR3 and MyD88 pathways⁷⁹. Our studies
7 also showed that TLR9-deficient NOD mice⁸⁰ and TRIF-deficient NOD mice⁸¹ are
8 protected from T1D development. LPS is the ligand of TLR4 and TRIF is one of the two
9 downstream signaling pathways of TLR4. It is interesting that diabetes protection in
10 TRIF-deficient NOD mice is mediated by gut microbiota⁸¹. Taken together, most TLRs
11 are required for T1D development in NOD mice, while TLR4 signaling regulates the
12 development of T1D through gut microbiota and/or LPS.

14 NLRs

15 Another family of PRR is the nucleotide-binding oligomerization domain-like
16 receptors (NLRs). These NLRs recognize both PAMPs and damage-associated
17 molecular patterns (DAMPs; molecules produced by stressed cells to promote an
18 inflammatory response). One of the best-studied NLRs is the nucleotide-binding
19 oligomerization domain-containing protein 2 (Nod2). Mutations in this receptor mediate
20 susceptibility to inflammatory bowel disease in humans^{82, 83}. We recently showed that
21 Nod2 also influences T1D development in NOD mice, mediated by altered gut
22 microbiota⁸⁴. In this study, *Nod2*^{-/-}NOD mice were protected from T1D only when
23 housed with other *Nod2*^{-/-}NOD mice. If the *Nod2*^{-/-}NOD mice were housed with Nod2-
24 sufficient wild-type NOD mice, the *Nod2*^{-/-}NOD mice developed a similar T1D incidence
25 to WT NOD mice. This provides important evidence that the environmental conditions
26 e.g. housing status can alter the interpretation of the disease phenotype in genetically
27 modified mouse strains in T1D studies.

28 The nucleotide-binding oligomerization domain, leucine-rich repeat and pyrin
29 domain-containing 3 (NLRP3) inflammasome is another protein involved in the detection
30 of pathogens by innate immune cells. We found reduced expression of chemokines and
31 chemokine receptors on both pancreatic islets and T cells in *NLRP3*^{-/-}NOD mice, which

protected the mice from developing T1D⁸⁵. It is currently unknown whether this process is modulated by the gut microbiota. The role of other NLR members in mediating T1D susceptibility is also unknown.

APC and gut microbiota interactions

Dendritic cells (DCs)

DCs are potent APCs found in both lymphoid and non-lymphoid tissue. Studies have shown that DCs are enriched at mucosal sites^{86, 87} and can sample microbial antigens from the gut lumen, presenting the antigens to the T cells and possibly B cells, residing in the mucosal tissue^{88, 89}. Mucosal DCs express a number of chemokine receptors and tissue homing adhesion molecules including CD103, all of which facilitate the intestinal DCs to migrate to other tissue sites after antigen uptake from the gut lumen^{90, 91}. DCs express a range of PRRs, and signaling through these induces maturation, promotes survival and maintains homeostasis within the DCs^{69, 92-98}. Thus, DCs are a pivotal component of the immune system, linking innate and adaptive immunity and inducing a specific immune response to pathogens but also to self-antigens in the context of autoimmunity.

In T1D, DCs present self-antigen and activate autoreactive T cells which damage and destroy pancreatic β -cells⁹⁹. DC activation through TLR9 and/or TLR3 has been shown to be important in enhancing IFN α secretion and thus promoting T cell activation and T1D development in NOD mice and humans^{100, 101}. Turley and colleagues have also shown that pancreatic draining lymph nodes (PLNs) function as an intersection for immune responses to gut non-self antigen and pancreatic self-antigen¹⁰². It is conceivable that some microbial antigens may share antigenic homology with pancreatic self-antigen, which can be sampled by intestinal DCs and promote undesirable autoimmune responses. In this regard, we have recently shown that autoreactive and diabetogenic CD8 T cells recognize a microbial peptide and promote the acceleration of T1D development in a T cell receptor (TCR) transgenic NOD mouse¹⁰³.

B cells

B cells originate and develop in the bone marrow. Mature B cells can differentiate to antibody-secreting plasma cells. IgM is the first antibody that B cells produce in response to pathogen invasion. However, IgM is usually low affinity and hence the need for affinity maturation including class switching, i.e., Ig gene rearrangements, to generate antibodies with high affinity, in order to more specifically target the antigen and control pathogen invasion¹⁰⁴⁻¹⁰⁶. B cells undergo class switching in response to different antigens. The type of class-switched antibody produced by B cells is also determined by the tissue location. For example, IgA is the predominant antibody in the mucosal tissues, while IgG is the most prevalent antibody in the circulation¹⁰⁷. B cells often require T cell help to complete class switching; however, commensal bacteria and/or bacterial antigens presented by mucosal DCs can induce B cells to secrete IgA, which protects the mucosa from invasion by pathogens and reduces inflammatory signals^{108, 109}. Intestinal epithelial cells can also induce IgA secretion¹¹⁰. In addition to antibody secretion, B cells also function as antigen presenting cells, promoting diabetes development¹¹¹⁻¹¹³. Although T1D is considered a T-cell mediated disease, it has become clear that B cells play an important role in the development of T1D. The precise role of B cells in the pathogenesis of T1D is complex and not fully understood; however, the autoantibodies produced by self-reactive B cells provide a very good biomarker to predict T1D onset in the individuals with high risk of developing T1D. The self-reactive B cells in T1D produce IgG autoantibodies to a range of antigens including insulin¹¹⁴, GAD¹¹⁵, IA-2¹¹⁶ and ZnT8¹¹⁷. Less is known about the role of IgA in T1D, although data from two T1D studies provide conflicting evidence as to whether the IgA concentrations in the serum are different between controls and T1D patients^{118, 119}. IgA is enriched in mucosal sites of both mouse and human in a secretory form and it is estimated that approximately 40 mg/kg body weight of IgA are produced in human intestine^{120, 121}. Detection of immunoglobulins bound to the bacteria within the intestine^{122, 123} may provide new avenues of investigation for T1D studies, enabling us to understand which gut microbiota become antibody targets and how the immune system interacts with them.

B cells in NOD mice express enhanced levels of some PRRs (and associated molecules) compared to C57BL/6 mice¹²⁴. Further, unmethylated CpG

1 deoxyoligonucleotides, which are a ligand for TLR9, activated pro-B cells. These cells
2 have a regulatory function and are capable of protecting NOD mice from T1D
3 development¹²⁵. Interestingly, the C1858T (lyp) polymorphism of the PTPN22 gene in
4 humans was also associated with altered B cell responses in individuals with T1D after
5 stimulation with CpG¹²⁶. Therefore, innate signals can mediate important changes
6 altering susceptibility to T1D in both NOD mice and humans. However, B cells are not
7 the only adaptive immune cells to be influenced by the gut microbiota.

9 **T Cells are influenced by gut microbiota**

10 T cells are a major player in the adaptive immune responses that both fight against
11 pathogens and regulate immune responses to maintain immuno-homeostasis. T cells
12 originate from bone marrow stem cells and undergo development in the thymus
13 (including the gene rearrangements that enable the antigen-specific TCR to be
14 expressed). Thymic T cells also undergo selection processes, ensuring the deletion of
15 highly auto-reactive T cells, which prevents autoimmunity. However, this process is not
16 complete and may contribute to the development of autoimmune disorders in people who
17 are susceptible to autoimmunity.

18 T cells expressing their antigen-specific TCR, can recognize a vast diversity of
19 antigens, pathogens and non-pathogens, which include self-antigens¹²⁷. However, the
20 antigens recognized by the TCR are presented by APCs through the antigenic peptide-
21 MHC complex. The APCs express costimulatory molecules and produce cytokines, and
22 these, together with the recognition of specific antigen, stimulate T cells to differentiate
23 into different effector subsets. Studies have shown that commensal bacteria, most likely
24 mediated by APCs, can induce T helper (Th) 1^{128, 129}, Th2^{130, 131}, Th17^{132, 133} and T
25 follicular helper (Tfh) cells¹³⁴. For example, the presence of Segmented Filamentous
26 bacteria (SFB) in the gut can induce IL17-producing CD4+ Th17 cells^{132, 133}, and Tfh
27 cells¹³⁴. Targeting SFB specifically may enable potential treatments for Th17-driven
28 autoimmune diseases e.g. Experimental Autoimmune Encephalomyelitis (EAE, a mouse
29 model of multiple sclerosis) and collagen-induced arthritis in mice^{135, 136}. Although, T1D
30 is driven by Th1 cells, SFB have been shown to protect NOD mice from T1D when
31 housed in SPF conditions¹³⁷. However, SFB introduction into GF NOD mice had no

effect on T1D development in female mice, whereas there was a significant delay in T1D onset in male GF mice after introducing SFB¹³⁸. Other studies have shown the inter-regulatory relationship between Th1 and Th17, where Th17 cells are also controlled by Treg cells. It is plausible that the Th1/Th17/Treg axis plays an important role in modulating T1D susceptibility by alteration of gut microbiota. The newly-identified role of SFB in altering Tfh differentiation and trafficking in a mouse model of arthritis is interesting¹³⁴. This provides evidence of the microbiota altering T:B cell interactions within the germinal centers prior to autoimmunity development. In T1D, Tfh T cells from diabetic NOD mice can transfer diabetes¹³⁹ and Tfh cells were found to be increased in T1D patients¹⁴⁰. A recent study investigating insulin-specific T:B cell interactions in NOD mice, also revealed an increase in Tfh cells associated with increased diabetes development¹⁴¹. Therefore further understanding antigen-specific germinal center interactions and the influence of gut microbiota, prior to autoimmunity development may be very important.

Treg cells

Tregs are characterized by their expression of the forkhead box transcription factor (FoxP3)¹⁴², and are potent at suppressing immune responses¹⁴³. Tregs were previously named suppressor T cells¹⁴⁴, and we have gained much more understanding of these cells in recent years. Tregs can be generated within the thymus (natural Tregs, nTregs) or in the periphery (induced Treg, iTregs). FoxP3 deficiency, caused by the Scurfy x-linked mutation¹⁴⁵, resulted in severe immune cell infiltration in multiple organs and autoimmune destruction^{146, 147}. Thus, Treg cells are vital in mediating immune tolerance to autoantigens. In addition, they are also very important in limiting the immune response to foreign antigens to prevent tissue damage.

Tregs, like other immune cells, also express TLRs including TLR4, TLR5, TLR7 and TLR8 as identified by real time PCR¹⁴⁸. Upon LPS stimulation, that is recognized via TLR4, Tregs became more activated and exhibit enhanced suppressive capabilities¹⁴⁸. Studies have shown that commensal bacteria, such as strains of *Clostridium*, by promoting a TGF- β rich environment, induce T effectors to become Tregs in the colon and protect mice from chemical induced colitis¹⁴⁹. Treg induction was also confirmed in

1 mice given a mixture of human stool-isolated *Clostridium* species¹⁵⁰. Interestingly, Treg
2 induction by *Clostridium* species was independent of PRR signaling, as Treg induction
3 was not impaired in a number of PRR deficient mice including *MyD88*^{-/-} mice¹⁴⁹.
4 However, other studies have shown that Treg conversion in colonized germ-free mice
5 with the altered Schaedler flora (ASF, a mixture of 8 strains of human gut bacteria
6 including a *Clostridium* species) is MyD88 dependent¹⁵¹. It is not clear whether other
7 strains of bacteria in the ASF also contribute to the Treg conversion. However, these
8 studies suggest that Treg induction and the mechanism behind it depend on the type of
9 bacteria. More recently, Nod2, a member of the NLR family, which recognizes the
10 bacterial component muramyl dipeptide (MDP) was also found to regulate human Treg
11 survival by preventing apoptosis induced by MDP stimulation; however, Tregs from
12 patients with IBD, who have the Nod2 gene mutation, were not protected from
13 apoptosis¹⁵². We have shown recently that Nod2-deficient NOD mice are protected from
14 T1D development, which was, at least in part, mediated by increased gut microbiota-
15 induced Tregs in the pancreatic lymph nodes⁸⁴. This data shows the microbiota and
16 immune recognition together shape the regulatory T cell response and may provide an
17 important target for therapy.

18 **Metabolism and the gut microbiota**

20 The intestinal microbiota utilize undigested food products as substrates for
21 fermentation resulting in the production of different metabolites. Short-chain fatty acids
22 (SCFAs), saturated fats, L-carnitine, and choline are examples of microbially-derived
23 metabolites. Therefore, the presence of these metabolites depends on the microbiota
24 composition. Studies have shown that the metabolites, especially SCFAs influence the
25 differentiation and function of immune cells; thus, they may play an important role in the
26 development of T1D.

27 Other metabolic components including sex hormones can affect the immune
28 system including the induction of autoimmunity. The female gender bias in T1D
29 development seen in the NOD mice has been shown to be consequent upon interactions
30 between sex hormones and gut microbiota^{138, 153}. The gut microbiota in male NOD mice
31 influence the levels of testosterone, and higher levels of testosterone are associated with

1 the protection against T1D development¹⁵³. Several human autoimmune disorders have a
2 strong gender bias, with a higher incidence in women. While human T1D in adulthood
3 has a small gender bias towards men, it is important to decipher the role(s) of hormones
4 and microbiota including microbial products in mediating susceptibility to autoimmune
5 diseases.

6 7 Metabolites

8 One of the most significant metabolites produced by gut microbiota are SCFAs,
9 during the fermentation of dietary fiber in the colon. Butyrate, propionate, and acetate
10 are the major SCFAs produced in the gut, which can regulate the host immune system,
11 central nervous system, gastrointestinal system, and metabolism through various
12 mechanisms. The oxidation of SCFAs, butyrate in particular, is the principal energy
13 source utilized by colonocytes^{154, 155}. Butyrate also enhances the integrity of human and
14 mouse intestinal epithelial cells. This occurs by controlling the assembly of tight
15 junctions as demonstrated in an *in vitro* culture system¹⁵⁶ and in mice *in vivo* through the
16 stabilization of the hypoxia-inducible factor (HIF), a transcription factor important for
17 mediating epithelial barrier functions¹⁵⁷. Moreover, butyrate can be sensed by the
18 immune system to promote Treg induction, concomitant with decreased inflammation in
19 the intestines¹⁵⁸⁻¹⁶⁰.

20 The short chain fatty acid propionate is converted into glucose in the intestine,
21 resulting in decreased glucose production from the liver¹⁶¹. Propionate also acts as an
22 agonist of FFAR3, inducing the peripheral nervous system to alter host metabolism by
23 decreasing adiposity, body weight and glucose production in the liver, thus promoting
24 better glucose control¹⁶². In addition, SCFAs can regulate the expression of peptide YY
25 (an enteroendocrine hormone) that controls gut motility and transit rate, as well as SCFA
26 uptake and can promote anti-inflammatory properties, offering protection from induced
27 inflammatory diseases such as colitis, arthritis and asthma in mouse models^{163, 164}. Thus,
28 increased production of SCFAs from dietary fiber supplements or the ingestion of
29 probiotics can inhibit pro-inflammatory cytokines and chemokines that could be used in
30 potential treatments for autoimmunity e.g. colitis. However, a balance would be

1 required, as SCFAs are an additional source of calories and can be associated with
2 obesity and metabolic syndrome¹⁶⁵.

3 While less is known about the role of SCFAs in the development of T1D, a few
4 recent studies have suggested that SCFAs can modulate T1D susceptibility. One study
5 showed that feeding NOD mice with acetylated or butyrate high-amylose maize starch
6 diets increased their serum concentrations of acetate or butyrate and protected NOD mice
7 from developing diabetes¹⁶⁶. Further, protection was enhanced if NOD mice were fed
8 with a combination of both acetylated and butyrate diets. Interestingly, NOD mice fed
9 with the high acetate diet had reduced frequencies and numbers of islet autoantigen-
10 reactive T cells in the spleen and pancreatic lymph nodes (PLNs). However, the
11 protection in NOD mice fed with a high butyrate-containing diet was related to increased
12 Treg number with enhanced suppressive functions¹⁶⁶. Another study demonstrated that
13 butyrate could influence the secretion of cathelicidin-related antimicrobial peptide
14 (CRAMP) by islets, with higher concentrations of CRAMP associated with protection
15 from T1D development¹⁶⁷. CRAMP expression was shown to alter the islet
16 microenvironment, by inducing tolerogenic islet macrophages, regulatory DCs and Tregs,
17 all of which facilitate the reduction of autoreactive T cell activation and thus prevent
18 diabetes development. Altering the microbiota composition by fecal transfer or by
19 antibiotic treatment can change the availability of metabolites, which in turn, alters the
20 risk of developing T1D^{168, 169}. Therefore, these options may prove useful in developing
21 prevention therapies. However, the relationship between microbial metabolism and
22 human T1D is still not well understood, and more studies in this area are needed in the
23 future.

24 **Diet and Type 1 Diabetes**

25 Diet is well known to influence microbial composition and functions. In Burkina
26 Faso, Africa, where diets consist of an abundance of complex carbohydrates resulting in
27 higher microbial diversity, children produce greater amounts of SCFAs when compared
28 to children from Europe¹⁷⁰. In contrast, GF mice colonized with human stool bacteria
29 from an individual with a Western-style diet had less microbial diversity and a worsened
30 ability to metabolize complex carbohydrates. However, those mice given the stool
31 bacteria from the individuals with an enriched microbiota-accessible carbohydrate diet

1 had increased microbial diversity and were able to metabolize complex carbohydrates¹⁹,
2 ¹⁷¹. Interestingly, numerous studies have suggested that *Prevotella:Bacteroides* ratios are
3 related to the dietary intake of either complex carbohydrate diets or proteins and fats
4 respectively^{170, 172}. Of note, when dietary fibers are almost completely fermented, the pH
5 of the large intestine increases, providing a reduction in butyrate-producing microbiota
6 but an increase in acetate- and propionate-producing *Bacteroides* bacteria¹⁷³.
7 A barley kernel-based bread diet was introduced to healthy subjects for 3 days in a recent
8 dietary intervention study¹⁷⁴. The authors identified the improvement of glucose
9 metabolism to be associated with an increased abundance of *Prevotella copri*¹⁷⁴. The
10 presence of *Prevotella* in these individuals had enhanced enzymatic activity related to
11 breaking down complex carbohydrates, which promotes the generation of a number of
12 SCFAs. The colonization of GF mice with microbiota from the study participants also
13 confirmed an increased abundance of *Prevotella* that was associated with improved
14 glucose metabolism. Furthermore, branched-chain fatty acid produced by the
15 fermentation of branched-chain amino acids correlated with insulin resistance in germ-
16 free mice receiving stool bacteria from obese human individuals¹⁷⁵.

17 Dietary influence on T1D has been examined both as a causative agent as well as
18 a preventative or modulating factor. Oral administration of nicotinamide, a vitamin B
19 group substance, to NOD mice prevented the development of diabetes¹⁷⁶. Further, NOD
20 mice were completely protected from T1D development when administered nicotinamide
21 in combination with a diet consisting of an infant formula, where soy was the source of
22 protein¹⁷⁷. Vitamin D, specifically the active form, 1,25 di-hydroxyvitamin D, has also
23 been shown to prevent from severe insulinitis due to the increased Treg cell activity¹⁷⁸⁻¹⁸⁰.
24 Gluten, a component of wheat protein, has many antigenic properties, and has been
25 implicated in the pathogenesis of several autoimmune disease states (predominantly CD)
26 but it has also been implicated in T1D. It has been reported that CD can affect up to
27 ~10% of individuals with T1D due to the overlap in *HLA-DR3/DQ2* genetic susceptibility
28 between the two diseases^{181, 182}. Furthermore, tissue transglutaminase antibodies are
29 present in some T1D patients, who share susceptibility SNPs to CD in the *CTLA4*
30 gene¹⁸³. Even in those individuals with T1D who were negative for the tissue
31 transglutaminase autoantibody in the serum, the antibody was still found in the

1 jejunum¹⁸⁴. Interestingly, T1D patients have increased expression of duodenal
2 inflammatory chemokines and cytokines compared to CD patients and healthy controls³².
3 This was also associated with altered microbiota in those T1D patients. Gluten-free diets
4 have been shown to protect NOD mice from the development of T1D¹⁸⁵⁻¹⁸⁷. Two studies
5 have shown that gluten in the diet affected the quantity and composition of the gut
6 microbiota^{185, 186}. Funda and colleagues also reported that while a gluten-free diet
7 prevented diabetes in NOD mice, a gluten-enriched diet also had a preventative
8 effect¹⁸⁷. They hypothesized that gluten itself is not diabetogenic but can have an
9 immunomodulatory effect on a diabetes-susceptible host by altering the gut microbiota
10 which in turn regulates the immune system. Human studies investigating how diet may
11 influence T1D susceptibility are currently underway. The BABYDIET study is a
12 prospective primary prevention trial recruiting children “at risk” of developing diabetes,
13 who have a first-degree relative with T1D and carry a T1D-risk HLA genotype. Children
14 were randomly assigned to one of two groups whereby gluten was introduced in the diet
15 at 6 months or 1 year of age¹⁸⁸. Data from the participants within the first 3 years of age
16 showed similar prevalence of islet autoimmunity regardless of when gluten was
17 introduced; however, these children will continue to be followed over time, to observe
18 generation of autoantibodies and other markers that are associated with the development
19 of both celiac and T1D autoimmunity.

20 21 22 **Antibiotic usage and Type 1 Diabetes** 23

24 There are many different classes of antibiotics that target different bacterial
25 pathogens. In addition to clearing the pathogen(s) from the original infection in various
26 body sites, antibiotics can alter the gut microbiota directly, particularly as most of the
27 antibiotics are taken via oral route. Will antibiotic usage affect T1D development by
28 changing gut microbiota? Studies in mouse models of T1D suggest that the type of
29 antibiotics, time of usage (early in life or later in life) and the duration of usage can
30 modify the susceptibility of T1D development. Table 1 summarizes different studies
31 conducted to assess the role of microbial modulation in the development of T1D in NOD

1 mice. We have shown that vancomycin, which predominantly targets Gram-positive
2 bacteria, promoted T1D development in NOD mice, whereas neomycin, which targets
3 Gram-negative bacteria, protected NOD mice from T1D development^{189, 190}.
4 Interestingly, others have reported that life-long vancomycin usage protected NOD mice
5 from T1D development¹⁹¹. It is clear that not all antibiotics have the same impact on
6 T1D development. Some antibiotics can protect NOD mice from the development of
7 T1D¹⁸⁹⁻¹⁹¹, while others promote the development of diabetes in NOD mice^{168, 192, 193}.
8 Interestingly, we found that the treatment of combination of four different antibiotics
9 (ampicillin, vancomycin, metronidazole and neomycin, AVMN) had no effect on
10 diabetes development in NOD mice despite the fact that the AVMN treatment depleted
11 most, if not all, gut bacteria (Peng, *et al.*, unpublished). This highlights the observation
12 that the treatment protocol can also influence diabetes development. In the study
13 showing that vancomycin protected NOD mice, the mice were treated from birth to 28
14 days of age or from 8 weeks of age to termination¹⁹¹. However, in the studies showing
15 that vancomycin accelerated T1D development, NOD mice were treated from conception
16 to termination or from conception to 24 hours post-birth^{190, 193}. The different treatment
17 protocols, including dose, duration and starting age for these antibiotic studies make it
18 difficult to compare the outcome of different studies directly. Moreover, the gender of
19 the mice used in the studies may also affect diabetes development. As discussed earlier,
20 sex hormones influence the gut microbiota and T1D susceptibility in the NOD mouse^{138,}
21 ¹⁵³. While most studies have used female mice, some studies have been conducted in
22 both genders. Candon and co-authors found that long-term (from conception to the
23 progeny at 40 wks of age) treatment with vancomycin or a combination of streptomycin,
24 colistin and ampicillin (Strep-Col-Amp) significantly increased diabetes development in
25 male NOD mice but had no effect on female mice¹⁹³. In another study, male NOD mice
26 receiving tylosin also exhibited increased diabetes development¹⁶⁸. Interestingly, the
27 female NOD mice, also exhibited increased diabetes development in one animal facility
28 but this was not reproducible in a second animal facility. This raises an important point
29 that the resident gut microbiota and animal facility standards can influence the
30 experimental outcome. This also raises the issue of reproducibility of studies as small
31 microbial changes may influence the effectiveness of the antibiotic treatment. Clearly,

these studies are not possible in humans; however, epidemiological investigations into antibiotic usage and T1D development in humans have not shown any evidence that antibiotics administered to children have influenced the onset of T1D.

Future Directions: Manipulating the gut microbiota as a novel therapy

Probiotics

Probiotics are microorganisms that may have health benefits by modifying the gut microbiota and improve nutrient absorption, enhance immune regulation and protect the host from infection and disease¹⁹⁴. While many of the probiotics may not colonize their hosts in the long-term, they do have important immunomodulatory effects in the short-term¹⁹⁵.

Probiotics have been shown to protect NOD mice and BB rats from developing T1D¹⁹⁶⁻¹⁹⁹. *Lactobacillus casei*, which is believed to be a probiotic strain, can protect NOD mice from T1D development when administered in the diet from 4 weeks of age¹⁹⁶. This protection was associated with decreased splenic CD8 T cell number and increased IL-10 and IL-2 cytokines with age. The probiotic VSL#3 is a mixture of bifidobacteria (*B. longum*, *B. infantis* and *B. breve*), lactobacilli (*L. acidophilus*, *L. casei*, *L. delbrueckii subsp. L. bulgaricus* and *L. plantarum*) and a strain of streptococcus bacteria (*Streptococcus salivarius subsp. thermophilus*)¹⁹⁷. In a study, Calcinaro and colleagues administered VSL#3 to NOD mice, three times per week from 4 to 32 weeks of age and this protocol led to significant protection from T1D development in treated NOD mice compared to non-treated controls (21% vs 81% respectively). VSL#3 administration decreased expression of IL-1 β and increased expression of indoleamine 2,3-dioxygenase and IL-33, both of which have tolerogenic properties¹⁹⁹. However, in another study, VSL#3 was administered via the drinking water to pregnant mice, just before birth until termination of the progeny (22 wks old), and this did not protect NOD mice from the development of T1D¹⁶⁹. In a very recent study, Hanninen and colleagues reported that *Akkermansia muciniphila* abundance is negatively correlated to T1D development and oral transfer of *A. muciniphila* delays diabetes development in NOD/Jax mice that, otherwise, have an early disease onset²⁰⁰. However, *A. muciniphila* did not reduce the

overall incidence of diabetes²⁰⁰, whereas gavage of *Clostridium butyricum* CGMCC0313.1 was able to significantly reduce the incidence of diabetes in NOD mice by promoting regulatory T cells²⁰¹.

There have been some studies investigating probiotics and host immunity in humans. Treating CD children with two *Bifidobacterium breve* strains, Primec and co-authors identified changes in microbiota composition that were associated with the changes in SCFAs and reduced TNF α in circulation²⁰². The authors also found that *Verrucomicrobia*, *Parcibacteria* and some other bacteria yet unknown phyla were strongly correlated to TNF α ²⁰². The probiotic administration to the CD children lowered the level of TNF α and reduced the abundance of *Verrucomicrobia*²⁰². This may provide potential therapeutic targets for CD. However, in a different disease setting, a reduced proportion of *Verrucomicrobia* has also been associated with glucose intolerance in type 2 diabetes patients and prediabetes subjects²⁰³. There have also been a few studies in T1D. A double-blind randomized pilot study investigated how *Lactobacillus johnsonii* N6.2, which was shown to delay T1D onset in BB rats¹⁹⁸, affects the host immunity in healthy adults²⁰⁴. In this phase I human study, only healthy individuals without gastrointestinal disorders or other health issues (e.g. diabetes, mental diseases, kidney and heart diseases and others) were recruited for the study. The administration of *L. johnsonii* N6.2 (taken in capsules for over 8 weeks) resulted in an increase of tryptophan in the circulation²⁰⁴. It is known that tryptophan promotes Treg cell induction and expansion as well as suppresses the differentiation of Th1 cells. These data suggest that *L. johnsonii* N6.2 is safe for treatment in adults, although the authors found that the study subjects had increased monocytes, NK cells and CD8 T cells in the peripheral blood compared to the placebo controls²⁰⁴. It is clear that more studies need to be done before launching clinical trials in the subjects with T1D or those at risk of developing T1D.

The Environmental Determinants of Diabetes in the Young (TEDDY) study follows children at risk of developing T1D to understand how different environmental factors may influence T1D susceptibility in humans. Recent data from the TEDDY study have revealed a large variability in the fecal microbial probiotic (total lactobacilli and *L. plantarum*) compositions between the children, particularly before 10 months of age²⁰⁵. It is currently unknown whether those with a reduced abundance of lactobacilli in early

1 life will have a greater risk of developing T1D; however, the TEDDY study shows the
2 presence of probiotic-related bacteria in children who are at risk of developing T1D, and
3 correlating this with development of diabetes, over time, will be of considerable interest.
4 This is an ever-expanding area with more probiotic-based human T1D clinical trials
5 planned.

7 Fecal Microbiota Transplantation

8 Fecal microbiota transplantation (FMT) can change the gut microbiota in the
9 recipients to elicit health benefits. FMT involves processing stool from a healthy donor
10 (for allogeneic transplants) or from the recipient (autologous transplant), although more
11 often the FMT is an allogeneic transplant from a healthy donor. Sometimes the FMT
12 recipients may need to be treated with antibiotics 24-72 hours prior to FMT to eliminate
13 any existing deleterious gut microbiota. An alternative approach to fast, and have bowel
14 preparaton shortly before the treatment. FMT has been used for the treatment of severe
15 *Clostridium difficile*-induced colitis²⁰⁶. Many studies confirmed that FMT therapy is safe
16 and effective in treating human IBD²⁰⁷. Interestingly, FMT (from lean donor feces)
17 improves insulin sensitivity in individuals with metabolic syndrome²⁰⁸.

18 In T1D, promising results using FMT have been shown in mice. Our study
19 showed that fecal materials from *MyD88*^{-/-}NOD mice, which were protected from
20 diabetes, can delay and reduce diabetes development in NOD mouse recipients²⁰⁹
21 However, there has been no report to date on whether FMT could be beneficial in
22 ameliorating disease in T1D patients or in preventing T1D development in the individuals
23 who are at risk of developing T1D. Both NOD mouse studies and recent TEDDY studies
24 have pointed to early life as an important window of opportunity for effective
25 intervention to reduce islet autoimmunity, especially in relation to the composition of gut
26 microbiota⁵⁶ and possibly FMT.

28 Concluding remarks

30 Increasing evidence suggests that there are microbial perturbations in individuals
31 with islet autoimmunity or T1D compared to healthy control subjects; however, we are

1 still not clear about the defined mechanisms. Therefore, further functional studies are
2 needed, not only to probe the interaction of microbiota with immune system but also to
3 identify the causal link(s) between the presence of certain gut bacteria and diabetogenic
4 autoimmune responses. Germ-free NOD mice will provide a valuable tool in deciphering
5 the role of the microbiota in relation to the development of T1D, both *in vitro*, and more
6 importantly, *in vivo*. While GF mice are known to have a less mature immune system,
7 particularly in relation to the gut-associated mucosal lymphoid tissue²¹⁰, GF NOD mice,
8 still develop T cell-mediated T1D^{71, 138, 153, 211}. Thus, using these GF NOD mice as
9 recipients for human stool from diabetic donors and healthy control donors, allows us to
10 understand how the microbiota may modulate the immune system in T1D *in vivo*.
11 Studies in obesity and T2D have shown that human gut microbiota can improve glucose
12 control and insulin resistance and thus manipulation of the microbiota may also be used
13 to achieve better glycemic control in patients with T1D.

14 Diet and probiotics may provide easier acceptance and compliance in participants
15 for disease prevention and/or intervention and/or modulation of disease. However, there
16 are still some challenges e.g. in dietary interventions, the subjects have to be at the age of
17 taking solid food. As for the use of probiotics, the question remains as to how long the
18 beneficial immunomodulatory effects induced by probiotic will last and if further doses
19 are required. Moreover, while FMT may alter the gut microbiota in the longer term,
20 many of these studies pre-treat with antibiotics which provides a niche allowing newly
21 introduced microbiota to colonize. It is noteworthy that antibiotic treatment may lead to
22 antibiotic resistance. In addition, it is highly possible that FMT-induced microbiota
23 changes can be modified by diet and other factors. Therefore, for future therapy
24 development, we require further understanding of 1) microbial community interactions as
25 a complex ecosystem; 2) the interaction of host microbiome with intestinal micro-
26 environment including gut epithelial cells and specialized gut endocrine cells including
27 Goblet cells and Paneth cells and 3) the interaction of gut microbiota with the host
28 immune cells locally and systemically. Furthermore, we also need to better define
29 subgroups of patients, as increasing evidence suggests that T1D is not a homogenous
30 disease condition. If we can combine the information on microbiota with clinical data, to
31 truly decipher the results by subgrouping patients based on resident microbiota

1 prevalence, c-peptide concentrations, autoantibody presence and type, as well as
2 autoreactive T cell information, we will be able to design treatment with more precision.
3 In summary, the role of microbiota in T1D is complex. While there are associations with
4 microbial composition changes at the time of seroconversion and changes associated with
5 disease onset, it remains unclear if the microbiota play a causal role in human T1D
6 development. However, studies in NOD mice have shown that microbial antigens
7 stimulated diabetogenic CD8 T cells and accelerated T1D development^{103, 212}. It is clear
8 from mouse and human studies, the microbiota can induce both proinflammatory and
9 anti-inflammatory changes of the immune system.

10

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